NCBI   results of **BLAST**

BLASTX 2.2.8 [Jan-05-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1082491251-5369-38913976047.BLASTQ3

Query=
          (1578 letters)

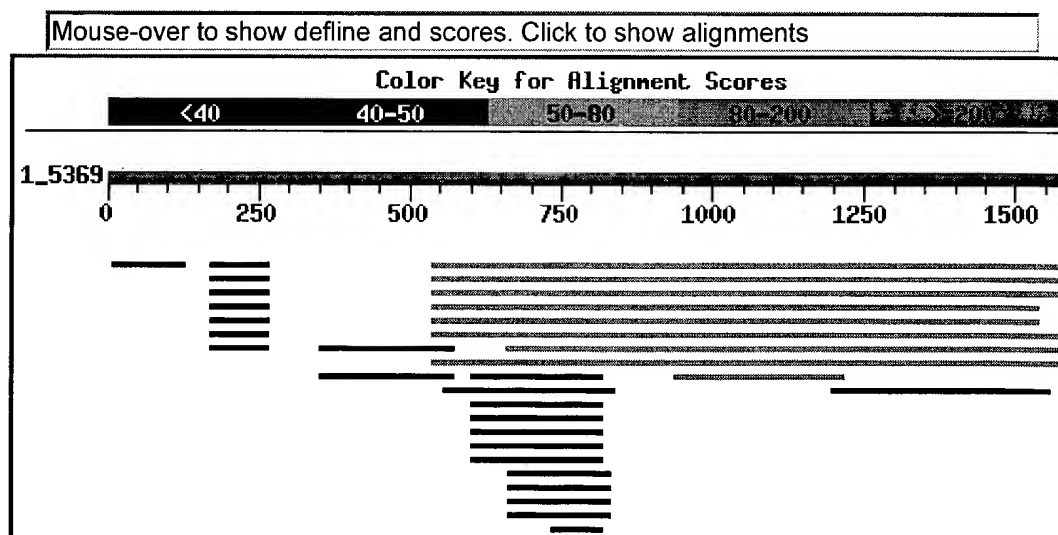**Database**: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
          2,768,312 sequences; 778,115,222 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 64 Blast Hits on the Query Sequence

Sequences producing significant alignments:	Score (bits)	E Value
gi|17999520|ref|NP_542119.1| vesicular inhibitory amino aci...	76	5e-25
gi|29428243|sp|Q95KE2|VIAA_MACFA Vesicular inhibitory amino...	75	1e-24
gi|29428127|sp|O35633|VIAA_MOUSE Vesicular inhibitory amino...	73	4e-23

gi|26665359|dbj|BAC44888.1| vesicular GABA transporter a fo...   73   4e-23
gi|13929106|ref|NP_113970.1| vesicular inhibitory amino aci...   72   6e-23
gi|6678569|ref|NP_033534.1| vesicular inhibitory amino acid...   73   4e-22
gi|34785016|gb|AAH36458.2| VIAAT protein [Homo sapiens]   69   2e-21
gi|34785895|gb|AAH57733.1| MGC68938 protein [Xenopus laevis]   59   2e-17
gi|19744862|gb|AAL96689.1| solute carrier family 32 member ...   57   1e-06
gi|31793484|ref|NP_855977.1| POSSIBLE CONSERVED MEMBRANE PR...   37   ·1.0
gi|41353676|emb|CAE55465.1| POSSIBLE CONSERVED MEMBRANE PRO...   37   1.0
gi|17368397|sp|P97260|SCAP_CRIGR   Sterol regulatory element ...   37   1.8
gi|40254240|ref|NP_766336.2| hypothetical protein 6030430O1...   37   1.8
gi|26327313|dbj|BAC27400.1| unnamed protein product [Mus mu...   37   1.8
gi|31418626|gb|AAH53109.1| 6030430O11 protein [Mus musculus]   37   1.8
gi|42734337|ref|NP_061958.1| hypothetical protein DKFZp434K...   36   2.3
gi|21758894|dbj|BAC05410.1| unnamed protein product [Homo s...   36   2.3
gi|34859315|ref|XP_219356.2| similar to hypothetical protei...   36   3.0
gi|44624381|gb|EAK56287.1| unknown [environmental sequence]   36   3.0
gi|115206|sp|P11586|C1TC_HUMAN   C-1-tetrahydrofolate synthas...   36   3.0
gi|13699868|ref|NP_005947.2| methylenetetrahydrofolate dehy...   36   3.0
gi|30048109|gb|AAH50420.1| Methylenetetrahydrofolate dehydr...   36   3.0
gi|37805836|dbj|BAC99471.1| hypothetical protein [Oryza sat...   35   4.0
gi|19850913|gb|AAL99692.1| C1-tetrahydrofolate synthase [Mu...   34   8.8
gi|111430|pir||A35367   methylenetetrahydrofolate dehydrogena...   34   8.8
gi|26335437|dbj|BAC31419.1| unnamed protein product [Mus mu...   34   ,8.8
gi|11968082|ref|NP_071953.1| C1-tetrahydrofolate synthase [...   34   8.8
gi|26348793|dbj|BAC38036.1| unnamed protein product [Mus mu...   34   8.8
gi|34871548|ref|XP_222019.2| similar to RIKEN cDNA 9430031J...   34   8.8
gi|37537544|ref|NP_780730.2| RIKEN cDNA 6430598A04 gene [Mu...   34   8.8
gi|26328379|dbj|BAC27928.1| unnamed protein product [Mus mu...   34   8.8
gi|40363747|dbj|BAD06308.1| vesicular GABA transporter [Cio...   30   9.6

Alignments

[Get selected sequences]   [Select all]   [Deselect all]

☐ >gi|17999520|ref|NP_542119.1| vesicular inhibitory amino acid transporter; GAB
        transporter; vesicular GABA transporter [Homo sapiens]
gi|29428257|sp|Q9H598|VIAA_HUMAN   Vesicular inhibitory amino acid transporter (GAB
        transporter) (Vesicular GABA transporter) (hVIAAT)
gi|13396317|emb|CAC15529.2| bA122O1.1 (A novel protein (ortholog of the mouse v
        inhibitory amino acid transporter, VIAAT)) [Homo sapiens]
gi|16549700|dbj|BAB70846.1| unnamed protein product [Homo sapiens]
gi|17975777|gb|AAK98782.1| vesicular inhibitory amino acid transporter [Homo sa
gi|31566392|gb|AAH53582.1| Vesicular inhibitory amino acid transporter [Homo sa
        Length = 525

Score = 76.3 bits (186), Expect(2) = 5e-25
Identities = 95/314 (30%), Positives = 106/314 (33%), Gaps = 101/314 (32%)
Frame = +1

```
Query: 580   FARMGFQAATDEEXXXXXXXXXXXXXDE------------SPAGTRALKRP-------SR 699
             FARMGFQAATDEE          +               P G    + P       R
Sbjct: 28    FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAEGEPCGDEGAEAPVEGDIHYQR 87

Query: 700   GSGAPLPPSGSKD-IRGPRQAQNH---------GVGAPSRACSCWAYPTP--------- 819
             GSGAPLPPSGSKD + G  +  H         G  +     +    P
Sbjct: 88    GSGAPLPPSGSKDQVGGGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820   GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-----------------R 939
             GLFLIIFAA                                S
Sbjct: 148   GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN 207

Query: 940   VAQIIELVMTCILPHV-------QQLPGA----------ARVAARPCCCLA---PSLRTS 1059
             VAQIIELVMTCIL  V       PG          A    PC L      + S
Sbjct: 208   VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060  LLCTLAHFVINIL--------------------SSPRLGLGEGQVLPSPLASSCSATRL 1176
             LLCTLAHFVINIL                  +  +  G ++ S   S      L
Sbjct: 268   LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177  RGNMQQPSEFHCMM 1218
              GNMQQPSEFHCMM
Sbjct: 327   EGNMQQPSEFHCMM 340
```

 Score = 76.3 bits (186), Expect = 2e-12
 Identities = 88/262 (33%), Positives = 99/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

```
Query: 537   SKLSNVATSVSNKS-VRQDG-FXXXXXXXXXXXXXXXXXXXC-----------------R 656
             SKLSNVATSVSNKS  +  G F                   C
Sbjct: 7     SKLSNVATSVSNKSQAKMSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAE 66

Query: 657   *EPCGDEGAEAPVE----RQRSSSAALRLQGHS---------GATTSPKSRR-------G 776
             EPCGDEGAEAPVE     QR S A L  G          G     PK
Sbjct: 67    GEPCGDEGAEAPVEGDIHYQRGSGAPLPPSGSKDQVGGGGEFGGHDKPKITAWEAGWNVT 126

Query: 777   SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA---------------RW 896
             +AIQGMFVLGLPYA +   +L    ++  A   T ++  A                 +
Sbjct: 127   NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY 186

Query: 897   WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC---------------------- 1007
              AIANACCAPRFPT        G  V+ A       C
Sbjct: 187   VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008  --PCRSTAVLLPCAFLKNLSAV 1067
               +TAVLLPCAFLKNL AV
Sbjct: 242   SWSIIATAVLLPCAFLKNLKAV 263
```

 Score = 69.7 bits (169), Expect = 2e-10
 Identities = 118/441 (26%), Positives = 134/441 (30%), Gaps = 152/441 (34%)
 Frame = +2

```
Query: 620   DDLDFEHRQGLQMXXXXX---------XXXXXXXXXXXXXXXCRPPAPRT----------- 739
             DDLDFEHRQGLQM                            P P +
Sbjct: 48    DDLDFEHRQGLQMDILKAEGEPCGDEGAEAPVEGDIHYQRGSGAPLPPSGSKDQVGGGGE 107
```

```
Query: 740   FGGHDKPKITAWERH---------------PGHVRAGPTLRRGCFXXXXXXXX------- 853
             FGGHDKPKITAWE           P   +   G   L  G F
Sbjct: 108   FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854   XXXXXYEENEDGEVV-------GHSQRLLRPALPN----A*XXXXXXXXXXASC------- 979
                  YEENEDGEVV           +       P   P              +C
Sbjct: 166   LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980   --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS--------------- 1096
               LMYNSFPGLPVSQ      A A+ LP     CA        ++S
Sbjct: 226   GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097  ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                   RDWAWEKVKFY            + + +  Q+ +
Sbjct: 281   VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199  XXXXXXXXXVLKGLFALVAYXXXXXXXX----------XXXXXXXXXXXXXXXXXXXSLP--- 1339
                     VLKGLFALVAY                                      LP
Sbjct: 341   NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFA 400

Query: 1340  -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS---------------- 1447
                    SLFQEGSRAFFPA       D  L++        T  RC+
Sbjct: 401   AVEVLEKSLFQEGSRAFFPA--CYSGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448  --------WASPLCFLLPSLF 1486
                     +  LCFLLPSLF
Sbjct: 456   LMGLTGSLTGAGLCFLLPSLF 476
```

```
Score = 62.8 bits (151), Expect(2) = 5e-25
Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
Frame = +3

Query: 1254  TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
             T EVITDNLPGSIRA      +++ A+L                    R+    A
Sbjct: 366   TKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYSGD 425

Query: 1374  RPLKSWGLTLRCALVHLCAALRAAHGPH----------PSVSCC---PASF-------T 1490
                LKSWGLTLRCALV +    L A + PH            C   P+  F
Sbjct: 426   GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491  CAWHQVFFDVAIFVIG 1538
                WHQVFFDVAIFVIG
Sbjct: 485   LLWHQVFFDVAIFVIG 500
```

```
Score = 35.8 bits (81), Expect = 3.0
Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
Frame = +1

Query: 1417  SIYVPHFALLMGLTPLFLAA-------------------QPLXXXXXXXXXXXXXXXXXXX 1536
             +IYVPHFALLMGLT        A
Sbjct: 447   AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537  XFVHSLEGLIEAYR 1578
              FVHSLEGLIEAYR
Sbjct: 507   GFVHSLEGLIEAYR 520
```

☐ >gi|29428243|sp|Q95KE2|VIAA_MACFA   Vesicular inhibitory amino acid transporter (G
         transporter) (Vesicular GABA transporter)
  gi|14388326|dbj|BAB60726.1| hypothetical protein [Macaca fascicularis]
         Length = 525

 Score = 75.5 bits (184), Expect(2) = 1e-24
 Identities = 96/314 (30%), Positives = 106/314 (33%), Gaps = 101/314 (32%)
 Frame = +1

Query: 580   FARMGFQAATDEEXXXXXXXXXXXXXDE-------------SPAGTRALKRP-------SR 699
             FARMGFQAATDEE   +   P G   + P   R
Sbjct: 28   FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAEGEPCGDEGAEPPVEGDIHYQR 87

Query: 700   GSGAPLPPSGSKDIRG----------PR-QAQNHGVGAPSRACSCWAYPTP--------- 819
             GSGAPLPPSGSKD G   P+ A   G   +   +   P
Sbjct: 88   GSGAPLPPSGSKDQVGAGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820   GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-------------------R 939
             GLFLIIFAA   S
Sbjct: 148   GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN 207

Query: 940   VAQIIELVMTCILPHV-------QQLPGA----------ARVAARPCCCLA---PSLRTS 1059
             VAQIIELVMTCIL V   PG   A   PC L   + S
Sbjct: 208   VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060 LLCTLAHFVINIL---------------------SSPRLGLGEGQVLPSPLASSCSATRL 1176
             LLCTLAHFVINIL   + + G ++ S   S   L
Sbjct: 268   LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCMM 1218
              GNMQQPSEFHCMM
Sbjct: 327   EGNMQQPSEFHCMM 340

 Score = 73.6 bits (179), Expect = 1e-11
 Identities = 86/262 (32%), Positives = 97/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537   SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXC-----------------R 656
             SKLSNVATSVSNKS +   F   C
Sbjct: 7   SKLSNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKAE 66

Query: 657   *EPCGDEGAEAPVE----RQRSSSAALRLQGHS---------GATTSPKSRR-------G 776
              EPCGDEGAE PVE   QR S A L G   G   PK
Sbjct: 67   GEPCGDEGAEPPVEGDIHYQRGSGAPLPPSGSKDQVGAGGEFGGHDKPKITAWEAGWNVT 126

Query: 777   SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA----------------RW 896
             +AIQGMFVLGLPYA +   +L   ++ A   T ++   A   +
Sbjct: 127   NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY 186

Query: 897   WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC---------------------- 1007
             AIANACCAPRFPT   G V+ A   C
Sbjct: 187   VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
               +TAVLLPCAFLKNL AV
Sbjct: 242   SWSIIATAVLLPCAFLKNLKAV 263

```
Score = 72.4 bits (176), Expect = 3e-11
Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
Frame = +2

Query: 620    DDLDFEHRQGLQMXXXXXXXX------------XXXXXXXXXXXCRPP--------APRT 739
              DDLDFEHRQGLQM                                  PP        A
Sbjct: 48     DDLDFEHRQGLQMDILKAEGEPCGDEGAEPPVEGDIHYQRGSGAPLPPSGSKDQVGAGGE 107

Query: 740    FGGHDKPKITAWERH--------------PGHVRAGPTLRRGCFXXXXXXXX------- 853
              FGGHDKPKITAWE             P  +  G L  G F
Sbjct: 108    FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854    XXXXXYEENEDGEVV-------GHSQRLLRPALPN----A*XXXXXXXXXASC------- 979
                   YEENEDGEVV        +    P   P                    +C
Sbjct: 166    LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980    --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS---------------- 1096
                LMYNSFPGLPVSQ       A A+ LP    CA      ++S
Sbjct: 226    GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097   ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                    RDWAWEKVKFY           + + +  Q+ +
Sbjct: 281    VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199   XXXXXXXXVLKGLFALVAYXXXXXXXX----------XXXXXXXXXXXXXXXXXXSLP--- 1339
                      VLKGLFALVAY                                     LP
Sbjct: 341    NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFA 400

Query: 1340   -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS----------------- 1447
                     SLFQEGSRAFFPA    G D  L++        T RC+
Sbjct: 401    AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448   --------WASPLCFLLPSLF 1486
                      +  LCFLLPSLF
Sbjct: 456    LMGLTGSLTGAGLCFLLPSLF 476
```

```
Score = 62.4 bits (150), Expect(2) = 1e-24
Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
Frame = +3

Query: 1254   TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
              T EVITDNLPGSIRA     +++ A+L                        R+   A
Sbjct: 366    TKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374   RPLKSWGLTLRCALVHLCAALRAAHGPH----------PSVSCC---PASF-------T 1490
                LKSWGLTLRCALV +   L A + PH                 C   P+ F
Sbjct: 426    GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491   CAWHQVFFDVAIFVIG 1538
                 WHQVFFDVAIFVIG
Sbjct: 485    LLWHQVFFDVAIFVIG 500
```

```
Score = 35.8 bits (81), Expect = 3.0
```

```
Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
Frame = +1


Query: 1417  SIYVPHFALLMGLTPLFLAA-------------------QPLXXXXXXXXXXXXXXXXX 1536
             +IYVPHFALLMGLT        A
Sbjct: 447   AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506


Query: 1537  XFVHSLEGLIEAYR 1578
              FVHSLEGLIEAYR
Sbjct: 507   GFVHSLEGLIEAYR 520
```

☐ >gi|29428127|sp|O35633|VIAA_MOUSE 🄻 Vesicular inhibitory amino acid transporter
            transporter) (Vesicular GABA transporter) (mVIAAT)
            (mVGAT)

 gi|26665360|dbj|BAC44889.1| 🄻 vesicular GABA transporter b form [Mus musculus]
 gi|30354125|gb|AAH52020.1| 🄻 Viaat protein [Mus musculus]
            Length = 525

```
Score = 72.8 bits (177), Expect = 2e-11
Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)
Frame = +3

Query: 537   SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXXC----------------R 656
             SKL+NVATSVSNKS   +    F                   C
Sbjct: 7     SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE 66

Query: 657   *EPCGDEGAEAPVE----RQR---------SSSAALRLQGHSGATTSPKSRR-------G 776
              EPCGDEGAEAPVE    QR         S    A+  G  G    PK
Sbjct: 67    GEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVT 126

Query: 777   SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA---------------RW 896
             +AIQGMFVLGLPYA +   +L    ++  A     T ++  A                +
Sbjct: 127   NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY 186

Query: 897   WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC--------------------- 1007
              AIANACCAPRFPT         G  V+ A        C
Sbjct: 187   VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008  --PCRSTAVLLPCAFLKNLSAV 1067
               +TAVLLPCAFLKNL AV
Sbjct: 242   SWSIIATAVLLPCAFLKNLKAV 263



Score = 72.0 bits (175), Expect = 4e-11
Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
Frame = +2

Query: 620   DDLDFEHRQGLQMXXXXXXXXXXXXXXXXXXX-----------XXCRPP---------APRT 739
             DDLDFEHRQGLQM                              PP          A
Sbjct: 48    DDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740   FGGHDKPKITAWERH--------------PGHVRAGPTLRRGCFXXXXXXXXX------- 853
             FGGHDKPKITAWE              P  +  G  L  G F
Sbjct: 108   FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854   XXXXXYEENEDGEVV-------GHSQRLLRPALPN----A*XXXXXXXXXASC------- 979
```

```
                     YEENEDGEVV         +     P  P                    +C
Sbjct: 166  LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980  --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS--------------- 1096
              LMYNSFPGLPVSQ       A A+ LP    CA      ++S
Sbjct: 226  GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097 ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                  RDWAWEKVKFY            + + +  Q+ +
Sbjct: 281  VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXXVLKGLFALVAYXXXXXXXX---------XXXXXXXXXXXXXXXXXXXSLP--- 1339
                   VLKGLFALVAY                                LP
Sbjct: 341  NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFA 400

Query: 1340 -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS---------------- 1447
                   SLFQEGSRAFFPA    G D  L++      T RC+
Sbjct: 401  AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 --------WASPLCFLLPSLF 1486
                  +  LCFLLPSLF
Sbjct: 456  LMGLTGSLTGAGLCFLLPSLF 476
```

```
  Score = 70.1 bits (170), Expect(2) = 4e-23
  Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)
  Frame = +1

Query: 580  FARMGFQAATDEEXXXXXXXXXXXXDE-------------SPAGTRALKRPSRGS----- 705
            FARMGFQAATDEE            +               P G    + P  G
Sbjct: 28   FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQR 87

Query: 706  -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP------------------- 819
             GAPLPPSGSKD      +  G   P     + W
Sbjct: 88   GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820  GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ--------------------R 939
            GLFLIIFAA                            S
Sbjct: 148  GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN 207

Query: 940  VAQIIELVMTCILPHV-------QQLPGA-----------ARVAARPCCCLA---PSLRTS 1059
            VAQIIELVMTCIL  V       PG          A    PC L       + S
Sbjct: 208  VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060 LLCTLAHFVINIL--------------------SSPRLGLGEGQVLPSPLASSCSATRL 1176
            LLCTLAHFVINIL                      +  + G ++ S   S      L
Sbjct: 268  LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177 RGNMQQPSEFHCMM 1218
             GNMQQPSEFHCMM
Sbjct: 327  EGNMQQPSEFHCMM 340
```

```
  Score = 62.4 bits (150), Expect(2) = 4e-23
  Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
  Frame = +3

Query: 1254 TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
```

```
             T EVITDNLPGSIRA        +++ A+L                          R+    A
Sbjct: 366   TKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374  RPLKSWGLTLRCALVHLCAALRAAHGPH-----------PSVSCC---PASF-------T 1490
             LKSWGLTLRCALV +   L A + PH                     C    P+ F
Sbjct: 426   GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491  CAWHQVFFDVAIFVIG 1538
             WHQVFFDVAIFVIG
Sbjct: 485   LLWHQVFFDVAIFVIG 500
```

```
 Score = 35.8 bits (81), Expect = 3.0
 Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
 Frame = +1

Query: 1417  SIYVPHFALLMGLTPLFLAA--------------------QPLXXXXXXXXXXXXXXXXX 1536
             +IYVPHFALLMGLT      A
Sbjct: 447   AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537  XFVHSLEGLIEAYR 1578
             FVHSLEGLIEAYR
Sbjct: 507   GFVHSLEGLIEAYR 520
```

```
☐ >gi|26665359|dbj|BAC44888.1|    vesicular GABA transporter a form [Mus musculus]
            Length = 521

 Score = 72.8 bits (177), Expect = 2e-11
 Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537   SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXC----------------R 656
             SKL+NVATSVSNKS   +      F                 C
Sbjct: 7     SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE 66

Query: 657   *EPCGDEGAEAPVE----RQR---------SSSAALRLQGHSGATTSPKSRR-------G 776
             EPCGDEGAEAPVE      QR          S   A+   G   G   PK
Sbjct: 67    GEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVT 126

Query: 777   SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA---------------RW 896
             +AIQGMFVLGLPYA +   +L   ++ A    T ++  A                  +
Sbjct: 127   NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY 186

Query: 897   WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC--------------------- 1007
             AIANACCAPRFPT        G  V+ A        C
Sbjct: 187   VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241

Query: 1008  --PCRSTAVLLPCAFLKNLSAV 1067
               +TAVLLPCAFLKNL AV
Sbjct: 242   SWSIIATAVLLPCAFLKNLKAV 263
```

```
 Score = 72.0 bits (175), Expect = 4e-11
 Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
 Frame = +2
```

```
Query: 620   DDLDFEHRQGLQMXXXXXXXXXXXXXXXXX-----------XXCRPP---------APRT 739
             DDLDFEHRQGLQM                               PP          A
Sbjct: 48    DDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740   FGGHDKPKITAWERH---------------PGHVRAGPTLRRGCFXXXXXXXX------- 853
             FGGHDKPKITAWE                 P  +  G  L  G F
Sbjct: 108   FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854   XXXXXYEENEDGEVV-------GHSQRLLRPALPN----A*XXXXXXXXXASC------- 979
                  YEENEDGEVV       +      P   P      +C
Sbjct: 166   LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980   --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS--------------- 1096
               LMYNSFPGLPVSQ      A A+ LP    CA      ++S
Sbjct: 226   GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097  ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                   RDWAWEKVKFY            + + +  Q+ +
Sbjct: 281   VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199  XXXXXXXXVLKGLFALVAYXXXXXXXX----------XXXXXXXXXXXXXXXXXXSLP--- 1339
                     VLKGLFALVAY                                  LP
Sbjct: 341   NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFA 400

Query: 1340  -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS---------------- 1447
                    SLFQEGSRAFFPA    G  D  L++       T RC+
Sbjct: 401   AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448  --------WASPLCFLLPSLF 1486
                  + LCFLLPSLF
Sbjct: 456   LMGLTGSLTGAGLCFLLPSLF 476


  Score = 70.1 bits (170), Expect(2) = 4e-23
  Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)
  Frame = +1

Query: 580   FARMGFQAATDEEXXXXXXXXXXXXXDE-------------SPAGTRALKRPSRGS----- 705
             FARMGFQAATDEE             +              P G    + P   G
Sbjct: 28    FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQR 87

Query: 706   -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP------------------ 819
              GAPLPPSGSKD     + G   P    + W
Sbjct: 88    GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820   GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ------------------R 939
             GLFLIIFAA                            S
Sbjct: 148   GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN 207

Query: 940   VAQIIELVMTCILPHV-------QQLPGA----------ARVAARPCCCLA---PSLRTS 1059
             VAQIIELVMTCIL  V       PG          A      PC L       + S
Sbjct: 208   VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS 267

Query: 1060  LLCTLAHFVINIL--------------------SSPRLGLGEGQVLPSPLASSCSATRL 1176
             LLCTLAHFVINIL                    + + G ++ S   S        L
Sbjct: 268   LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326

Query: 1177  RGNMQQPSEFHCMM 1218
              GNMQQPSEFHCMM
```

```
Sbjct: 327   EGNMQQPSEFHCMM 340
```

```
 Score = 62.4 bits (150), Expect(2) = 4e-23
 Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
 Frame = +3
```

```
Query: 1254  TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
             T EVITDNLPGSIRA      +++ A+L                     R+    A
Sbjct: 366   TKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374  RPLKSWGLTLRCALVHLCAALRAAHGPH-----------PSVSCC---PASF-------T 1490
               LKSWGLTLRCALV +   L A + PH              C   P+ F
Sbjct: 426   GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491  CAWHQVFFDVAIFVIG 1538
                 WHQVFFDVAIFVIG
Sbjct: 485   LLWHQVFFDVAIFVIG 500
```

```
 □ >gi|13929106|ref|NP_113970.1|  🔲 vesicular inhibitory amino acid transporter [Rat
   gi|34860244|ref|XP_346679.1|  🔲 hypothetical protein XP_346678 [Rattus norvegicus]
   gi|29428082|sp|O35458|VIAA_RAT  🔲 Vesicular inhibitory amino acid transporter (GAB
              transporter) (Vesicular GABA transporter) (rGVAT)
   gi|2587061|gb|AAB82950.1|  🔲 vesicular GABA transporter [Rattus norvegicus]
              Length = 525
```

```
 Score = 72.0 bits (175), Expect = 4e-11
 Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
 Frame = +2
```

```
Query: 620   DDLDFEHRQGLQMXXXXXXXX-----------XXXXXXXXXXXCRPP---------APRT 739
             DDLDFEHRQGLQM                              PP          A
Sbjct: 48    DDLDFEHRQGLQMDILKSEGEPCGDEGAEPPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740   FGGHDKPKITAWERH---------------PGHVRAGPTLRRGCFXXXXXXXXX------- 853
             FGGHDKPKITAWE              P + G L G F
Sbjct: 108   FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854   XXXXXYEENEDGEVV--------GHSQRLLRPALPN----A*XXXXXXXXXASC------- 979
                  YEENEDGEVV          +    P P              +C
Sbjct: 166   LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980   --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS--------------- 1096
               LMYNSFPGLPVSQ      A A+ LP    CA      ++S
Sbjct: 226   GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097  ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                   RDWAWEKVKFY           + + +  Q+ +
Sbjct: 281   VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199  XXXXXXXXVLKGLFALVAYXXXXXXXX----------XXXXXXXXXXXXXXXXXXSLP--- 1339
                     VLKGLFALVAY                                      LP
Sbjct: 341   NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFA 400

Query: 1340  -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS---------------- 1447
                    SLFQEGSRAFFPA     G D L++        T RC+
```

```
Sbjct: 401  AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWGL---TLRCALVVFTLLMAIYVPHFAL  455

Query: 1448 --------WASPLCFLLPSLF  1486
                    + LCFLLPSLF
Sbjct: 456  LMGLTGSLTGAGLCFLLPSLF  476



 Score = 70.9 bits (172), Expect = 8e-11
 Identities = 84/262 (32%), Positives = 97/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537  SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXC----------------R  656
            SKL+NVATSVSNKS  +    F                   C
Sbjct: 7    SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE  66

Query: 657  *EPCGDEGAEAPVE----RQR---------SSSAALRLQGHSGATTSPKSRR-------G  776
             EPCGDEGAE PVE    QR         S  A+  G G    PK
Sbjct: 67   GEPCGDEGAEPPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVT  126

Query: 777  SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA----------------RW  896
            +AIQGMFVLGLPYA +   +L   ++ A   T ++ A                +
Sbjct: 127  NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY  186

Query: 897  WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC--------------------  1007
             AIANACCAPRFPT        G  V+ A       C
Sbjct: 187  VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK  241

Query: 1008 --PCRSTAVLLPCAFLKNLSAV  1067
              +TAVLLPCAFLKNL AV
Sbjct: 242  SWSIIATAVLLPCAFLKNLKAV  263



 Score = 69.7 bits (169), Expect(2) = 6e-23
 Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)
 Frame = +1

Query: 580  FARMGFQAATDEEXXXXXXXXXXXXXDE-------------SPAGTRALKRPSRGS-----  705
            FARMGFQAATDEE            +                P G   + P  G
Sbjct: 28   FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSEGEPCGDEGAEPPVEGDIHYQR  87

Query: 706  -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP------------------  819
             GAPLPPSGSKD     + G P   + W
Sbjct: 88   GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL  147

Query: 820  GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ-------------------R  939
            GLFLIIFAA                            S
Sbjct: 148  GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN  207

Query: 940  VAQIIELVMTCILPHV-------QQLPGA----------ARVAARPCCCLA---PSLRTS  1059
            VAQIIELVMTCIL V        PG             A    PC L     + S
Sbjct: 208  VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS  267

Query: 1060 LLCTLAHFVINIL--------------------SSPRLGLGEGQVLPSPLASSCSATRL  1176
            LLCTLAHFVINIL                    +  +  G ++ S  S      L
Sbjct: 268  LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL  326

Query: 1177 RGNMQQPSEFHCMM  1218
            GNMQQPSEFHCMM
```

```
Sbjct: 327   EGNMQQPSEFHCMM 340
```

```
 Score = 62.4 bits (150), Expect(2) = 6e-23
 Identities = 52/136 (38%), Positives = 60/136 (44%), Gaps = 41/136 (30%)
 Frame = +3

Query: 1254  TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
             T EVITDNLPGSIRA     +++ A+L                     R+    A
Sbjct: 366   TKEVITDNLPGSIRAVVNIFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425

Query: 1374  RPLKSWGLTLRCALVHLCAALRAAHGPH-----------PSVSCC---PASF-------T 1490
               LKSWGLTLRCALV +   L A + PH                  C  P+ F
Sbjct: 426   GRLKSWGLTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484

Query: 1491  CAWHQVFFDVAIFVIG 1538
                 WHQVFFDVAIFVIG
Sbjct: 485   LLWHQVFFDVAIFVIG 500
```

```
 Score = 35.8 bits (81), Expect = 3.0
 Identities = 27/74 (36%), Positives = 28/74 (37%), Gaps = 20/74 (27%)
 Frame = +1

Query: 1417  SIYVPHFALLMGLTPLFLAA--------------------QPLXXXXXXXXXXXXXXXXXX 1536
             +IYVPHFALLMGLT       A
Sbjct: 447   AIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRKLLWHQVFFDVAIFVIGGICSVS 506

Query: 1537  XFVHSLEGLIEAYR 1578
              FVHSLEGLIEAYR
Sbjct: 507   GFVHSLEGLIEAYR 520
```

```
 ☐ >gi|6678569|ref|NP_033534.1|   🔲 vesicular inhibitory amino acid transporter [Mus
   gi|2826776|emb|CAA04864.1|   🔲 vesicular inhibitory amino acid transporter [Mus mus
             Length = 521

 Score = 72.8 bits (177), Expect = 2e-11
 Identities = 85/262 (32%), Positives = 98/262 (37%), Gaps = 85/262 (32%)
 Frame = +3

Query: 537   SKLSNVATSVSNKSVRQDG--FXXXXXXXXXXXXXXXXXXXXC------------------R 656
             SKL+NVATSVSNKS   +     F                  C
Sbjct: 7     SKLTNVATSVSNKSQAKVSGMFARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSE 66

Query: 657   *EPCGDEGAEAPVE----RQR---------SSSAALRLQGHSGATTSPKSRR-------G 776
              EPCGDEGAEAPVE     QR          S   A+  G  G    PK
Sbjct: 67    GEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVT 126

Query: 777   SAIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA---------------RW 896
             +AIQGMFVLGLPYA +   +L    ++  A    T  ++  A              +
Sbjct: 127   NAIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSY 186

Query: 897   WAIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC---------------------- 1007
             AIANACCAPRFPT        G  V+ A      C
Sbjct: 187   VAIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQK 241
```

```
Query: 1008 --PCRSTAVLLPCAFLKNLSAV 1067
                +TAVLLPCAFLKNL AV
Sbjct: 242  SWSIIATAVLLPCAFLKNLKAV 263
```

```
 Score = 72.4 bits (176), Expect = 3e-11
 Identities = 120/441 (27%), Positives = 135/441 (30%), Gaps = 152/441 (34%)
 Frame = +2
```

```
Query: 620  DDLDFEHRQGLQMXXXXXXXXXXXXXXXXXX-----------XXCRPP---------APRT 739
            DDLDFEHRQGLQM                                PP           A
Sbjct: 48   DDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQRGGAPLPPSGSKDQAVGAGGE 107

Query: 740  FGGHDKPKITAWERH---------------PGHVRAGPTLRRGCFXXXXXXXX------- 853
            FGGHDKPKITAWE              P  +  G L G F
Sbjct: 108  FGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL--GLFLIIFAAVVCCYTGKI 165

Query: 854  XXXXXYEENEDGEVV-------GHSQRLLRPALPN----A*XXXXXXXXXASC------- 979
                 YEENEDGEVV          +     P  P              +C
Sbjct: 166  LIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELVMTCILYVVVS 225

Query: 980  --LMYNSFPGLPVSQHG---RAAALRLP*EPLCCALWPTSSSIS--------------- 1096
              LMYNSFPGLPVSQ      A A+ LP    CA      ++S
Sbjct: 226  GNLMYNSFPGLPVSQKSWSIIATAVLLP-----CAFLKNLKAVSKFSLLCTLAHFVINIL 280

Query: 1097 ------CPPRDWAWEKVKFY-----------HLHWHHRVQLHVSGXXXX---------XX 1198
                  RDWAWEKVKFY              + + + Q+ +
Sbjct: 281  VIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFSYTSQIFLPSLEGNMQQPSEFHCMM 340

Query: 1199 XXXXXXXXVLKGLFALVAYXXXXXXXX----------XXXXXXXXXXXXXXXXXXXSLP--- 1339
                    VLKGLFALVAY                                    LP
Sbjct: 341  NWTHIAACVLKGLFALVAYLTWADETKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFA 400

Query: 1340 -------SLFQEGSRAFFPAPEVLGADAALRARPFMCRTSRCS---------------- 1447
                   SLFQEGSRAFFPA  G D L++    T RC+
Sbjct: 401  AVEVLEKSLFQEGSRAFFPA--CYGGDGRLKSWEL---TLRCALVVFTLLMAIYVPHFAL 455

Query: 1448 --------WASPLCFLLPSLF 1486
                  + LCFLLPSLF
Sbjct: 456  LMGLTGSLTGAGLCFLLPSLF 476
```

```
 Score = 70.1 bits (170), Expect(2) = 4e-22
 Identities = 92/314 (29%), Positives = 101/314 (32%), Gaps = 101/314 (32%)
 Frame = +1
```

```
Query: 580  FARMGFQAATDEEXXXXXXXXXXXXXDE-------------SPAGTRALKRPSRGS----- 705
            FARMGFQAATDEE            +             P G   + P G
Sbjct: 28   FARMGFQAATDEEAVGFAHCDDLDFEHRQGLQMDILKSEGEPCGDEGAEAPVEGDIHYQR 87

Query: 706  -GAPLPPSGSKDIRGPRQAQNHGVGAPSRAC--SCWAYPTP------------------ 819
             GAPLPPSGSKD       + G P    + W
Sbjct: 88   GGAPLPPSGSKDQAVGAGGEFGGHDKPKITAWEAGWNVTNAIQGMFVLGLPYAILHGGYL 147

Query: 820  GLFLIIFAAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXSQ--------------------R 939
            GLFLIIFAA                                S
Sbjct: 148  GLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVN 207
```

```
Query: 940  VAQIIELVMTCILPHV-------QQLPGA----------ARVAARPCCCLA---PSLRTS 1059
            VAQIIELVMTCIL V       PG           A    PC  L      + S
Sbjct: 208  VAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKSWSIIATAVLLPCAFLKNLKAVSKFS 267


Query: 1060 LLCTLAHFVINIL--------------------SSPRLGLGEGQVLPSPLASSCSATRL 1176
            LLCTLAHFVINIL             + +  G ++ S   S      L
Sbjct: 268  LLCTLAHFVINILVIAYCLSRARDWAWEKVKFYIDVKKFPISIGIIVFS-YTSQIFLPSL 326


Query: 1177 RGNMQQPSEFHCMM 1218
             GNMQQPSEFHCMM
Sbjct: 327  EGNMQQPSEFHCMM 340
```

```
 Score = 59.3 bits (142), Expect(2) = 4e-22
 Identities = 51/136 (37%), Positives = 59/136 (43%), Gaps = 41/136 (30%)
 Frame = +3
```

```
Query: 1254 TSEVITDNLPGSIRAGQGAVVLSSAILC--------------------RRSSRKAAAPFS 1373
            T EVITDNLPGSIRA       +++ A+L                    R+    A
Sbjct: 366  TKEVITDNLPGSIRAVVNLFLVAKALLSYPLPFFAAVEVLEKSLFQEGSRAFFPACYGGD 425


Query: 1374 RPLKSWGLTLRCALVHLCAALRAAHGPH----------PSVSCC---PASF-------T 1490
             LKSW LTLRCALV +   L A + PH                    C   P+  F
Sbjct: 426  GRLKSWELTLRCALV-VFTLLMAIYVPHFALLMGLTGSLTGAGLCFLLPSLFHLRLLWRK 484


Query: 1491 CAWHQVFFDVAIFVIG 1538
               WHQVFFDVAIFVIG
Sbjct: 485  LLWHQVFFDVAIFVIG 500
```

```
□ >gi|34785016|gb|AAH36458.2|   L  VIAAT protein [Homo sapiens]
              Length = 475
```

```
 Score = 69.3 bits (168), Expect = 2e-10
 Identities = 71/201 (35%), Positives = 81/201 (40%), Gaps = 65/201 (32%)
 Frame = +3
```

```
Query: 660  EPCGDEGAEAPVE----RQRSSSAALRLQGHS---------GATTSPKSRR-------GS 779
            EPCGDEGAEAPVE    QR S A L  G         G   PK        +
Sbjct: 18   EPCGDEGAEAPVEGDIHYQRGSGAPLPPSGSKDQVGGGGEFGGHDKPKITAWEAGWNVTN 77


Query: 780  AIQGMFVLGLPYAGVVSHHLRRRCVLPRAC----TRRMKTA---------------RWW 899
            AIQGMFVLGLPYA +   +L   ++ A    T ++  A                  +
Sbjct: 78   AIQGMFVLGLPYAILHGGYLGLFLIIFAAVVCCYTGKILIACLYEENEDGEVVRVRDSYV 137


Query: 900  AIANACCAPRFPTRSADHRAGDDVHPASCTTASRGC----------------------- 1007
            AIANACCAPRFPT      G V+ A       C
Sbjct: 138  AIANACCAPRFPT-----LGGRVVNVAQIIELVMTCILYVVVSGNLMYNSFPGLPVSQKS 192


Query: 1008 -PCRSTAVLLPCAFLKNLSAV 1067
              +TAVLLPCAFLKNL AV
Sbjct: 193  WSIIATAVLLPCAFLKNLRAV 213
```

```
 Score = 64.3 bits (155), Expect(2) = 2e-21
 Identities = 81/256 (31%), Positives = 90/256 (35%), Gaps = 82/256 (32%)
```

Screenshot 1

RID=1082491251-5369-38913976047.BLASTQ3. - Microsoft Internet Explorer provided by USPTO

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Address http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

Distribution of 64 Blast Hits on the Query Sequence

BAC99471 hypothetical protein [Oryza sativa (japonica cultivar-gr..S=35.4 E=4.0

Color Key for Alignment Scores

<40   40-50   50-80   80-200

1_5369

0   250   500   750   1000   1250   1500

Sequences producing significant alignments:	Score (bits)	E Value
gi|17999520|ref|NP_542119.1| vesicular inhibitory amino aci...	76	5e-25
gi|29428243|sp|Q95KE2|VIAA_MACFA Vesicular inhibitory amino...	75	1e-24
gi|29428127|sp|O35633|VIAA_MOUSE Vesicular inhibitory amino...	73	4e-23
gi|26665359|dbj|BAC44888.1| vesicular GABA transporter a fo...	73	4e-23

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#37805836   Internet

Screenshot 2

RID=1082491251-5369-38913976047.BLASTQ3. - Microsoft Internet Explorer provided by USPTO

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Address http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi

Distribution of 64 Blast Hits on the Query Sequence

AAH50420 Methylenetetrahydrofolate dehydrogenase 1 [Homo sapiens]..S=35.8 E=3.0

Color Key for Alignment Scores

<40   40-50   50-80   80-200

1_5369

0   250   500   750   1000   1250   1500

Sequences producing significant alignments:	Score (bits)	E Value
gi|17999520|ref|NP_542119.1| vesicular inhibitory amino aci...	76	5e-25
gi|29428243|sp|Q95KE2|VIAA_MACFA Vesicular inhibitory amino...	75	1e-24
gi|29428127|sp|O35633|VIAA_MOUSE Vesicular inhibitory amino...	73	4e-23
gi|26665359|dbj|BAC44888.1| vesicular GABA transporter a fo...	73	4e-23

http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi#30048109   Internet

Distribution of 64 Blast Hits on the Query Sequence

NP_542119 vesicular inhibitory amino acid transporter; GABA and..S=76.3 E=5e-25

Sequences producing significant alignments:

	Score (bits)	E Value
gi|17999520|ref|NP_542119.1| vesicular inhibitory amino aci...	76	5e-25
gi|29428243|sp|Q95KE2|VIAA_MACFA Vesicular inhibitory amino...	75	1e-24
gi|29428127|sp|O35633|VIAA_MOUSE Vesicular inhibitory amino...	73	4e-23
gi|26665359|dbj|BAC44800.1| vesicular GABA transporter a fo...	73	4e-23